CHARACTERISATION OF THE TRANSCRIPTOMIC AND PROTEOMIC PROFILE OF ASTROCYTES IN MULTIPLE SCLEROSIS

By

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Submitted for the degree of Doctor of Philosophy (PhD)

Sheffield Institute for Translational Neuroscience
University of Sheffield

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Volume II

APPENDICES

Appendix I

The UK Multiple Sclerosis Tissue Bank

Division of Neuroscience and Mental Health
Imperial College London
Charing Cross Campus
Fulham Palace Road
London W6 8RF

Tel: 020 8846 7324
Fax: 020 8846 7500
E-mail: ukmstissuebank@imperial.ac.uk

Conditions for accepting post-mortem human material from the UK Multiple Sclerosis Tissue Bank

1. I accept samples of human material on the understanding that they will only be used for research, and that they are provided without warranty as to their properties or fitness for any particular purpose and without any other warranty whatsoever, expressed or implied.

2. I realise that the Tissue Bank does not screen the tissue or fluid that it procures for the presence of any infectious agents. I am aware of the potential risks in handling such material and hereby give assurance that all procedures employed in the handling, storage and use of the supplied material meet standards set by either Clinical Pathology Accreditation (UK) Ltd or the Health and Safety Executive. I and the Institution where I am based will indemnify and hold harmless the Multiple Sclerosis Society and Imperial College of Science Technology and Medicine against any damages, dispute or injury arising from a failure to maintain such safeguards.

3. I agree to be held responsible for the use of the material supplied to me. Under no circumstances will the samples be used for a project other than the one described in my application nor will they be sold or transferred to a third party without having obtained prior approval from the Tissue Bank.

4. I accept responsibility for gaining approval from the appropriate ethics committee for all work performed on material that I receive from the Tissue Bank – I understand that material will only be supplied once the Tissue Bank has received confirmation of this approval. I note that all procedures used by the Tissue Bank in the procurement, storage and distribution of tissue have been approved the relevant Multicentre Research Ethics Committee (**MREC/02/2/39**).

5. I will at all times abide by the ethical guidelines relating to the use of post-mortem human tissue for research purposes laid out by The Royal College of Pathologists in "Guidelines for the retention of tissue and organs at post-mortem examination, March 2000" (available at http://www.rcpath.org) and as may be amended from time to time.

6. I will provide a short written summary of the work performed on material supplied by the Tissue Bank one year after I have received the samples and on completion of the project. In addition, and upon request by the Multiple Sclerosis Society or Imperial College of Science, Technology and Medicine, I shall supply information on the use and fate of the material that I have received from the Tissue Bank, including the availability of any unused material.

continued...

Funded by the Multiple Sclerosis Society of Great Britain and Northern Ireland, Registered Charity 207495

Appendix I cont.

The UK Multiple Sclerosis Tissue Bank

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7. If work performed on material supplied by the Tissue Bank generates ideas, rights, processes or products of potential commercial value, I and the Institution where I am based will enter into a separate agreement with the Multiple Sclerosis Society and Imperial College of Science, Technology and Medicine on all relevant intellectual property issues.

8. I will not sell or transfer to a third party any intellectual property rights arising from work performed on material supplied by the Tissue Bank without written agreement from the Multiple Sclerosis Society and Imperial College of Science, Technology and Medicine.

9. I agree to cite the contribution made by the Tissue Bank in the "Materials and Methods" and "Acknowledgements" sections of all publications arising from research performed on material that it has supplied and will make available copies of such publications. The Tissue Bank should be acknowledged in the following manner:

   "Tissue (or cerebrospinal fluid) samples and associated clinical and neuropathological data were supplied by the UK Multiple Sclerosis Tissue Bank, funded by the Multiple Sclerosis Society of Great Britain and Northern Ireland, registered charity 207495."

   Members of the Tissue Bank may request co-authorship when the provision of tissue has required particularly time consuming protocols.

10. My right to undertake the obligations and give the undertakings detailed in this Agreement is confirmed by the signature of an authorised representative of the Institution of which I am an employee.

Signed: M. Nicola Woodroofe

Name: M NICOLA WOODROOFE

Date: 3/3/08

Signature on behalf of the Employer:

Signed:

Name: PJ HAYES

Date: 4.3.08

Position Held: DIRECTOR R&D

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Appendix I cont.

FOR SBTB OFFICE USE

Project no. ..11/002.....

AUTHORISATION TO USE TISSUE RESOURCE FROM THE SHEFFIELD BRAIN TISSUE BANK (SBTB)

FOLLOWING CONSIDERATION BY THE SBTB MANAGEMENT BOARD:

Proposed Study Title

.....

THE ROLE OF ASTROCYTES IN THE PATHOGENESIS OF MULTIPLE SCLEROSIS: A TRANSCRIPTOMIC & PROTEOMIC STUDY

.....

Head of proposed study

Title.....Dr..... Initials.....J.E.....

Surname.....Simpson.....

Position..... Lecturer.....

Organisation.... UNIVERSITY OF SHEFFIELD.....

Address..... Sheffield Institute of Translational Neuroscience (SITraN), University of Sheffield, 385A Glossop Road, SHEFFIELD, S10 2HQ,UK

Telephone No... 0114 22 22242... Fax No.. 0114 22 22290 .....

Email .... . julie.simpson@sheffield.ac.uk. .....

SBTB PROJECT REQUEST NUMBER: .....11/002.....

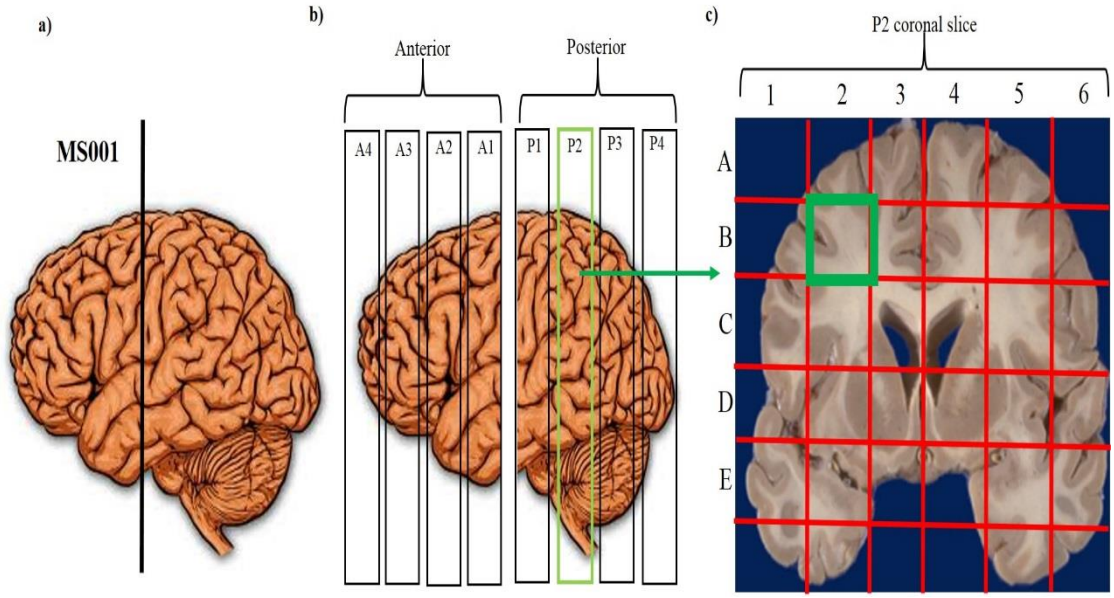
This project was reviewed by the SBTB Management Board and approval to release tissue under REC **08/MRE00/103** was granted.

Professor P G Ince
Director SBTB

Date: 20/6/2011

The majority of all cases used throughout this thesis were obtained from the UK MS Tissue Bank, only one case was obtained from the Sheffield Brain Tissue Bank used in Chapter 3.

Appendix II



An illustration of the brain slicing and preparation of tissue blocks by the UK Multiple Sclerosis Tissue Bank. The whole brain is divided in half (a), each half is cut into 1cm thick coronal brain slices and numbered based on whether they were cut anterior or posterior to the mammillary bodies (b). Each coronal slice is placed on a gird reference and cut into $2cm^2$ blocks, based on the coordinates of the cutting and case ID, each block can be distinguished and associated with a specific case and region of the brain, e.g block MS001 P2B2 (c, green box). Figure adapted from The UK MS tissue Bank (2008).

UK MS Society Tissue Bank (2008) Standard Operating procedure – Cutting and snap-freezing fresh brain slices.

Appendix II cont.

FFPE section block number region – UK Multiple Sclerosis Tissue Bank

1 Superior frontal gyrus

2 Cingulate gyrus

3 Nucleus accumbens

4 Caudate and putamen

5a Nucleus basalis Maynert

5b Globus pallidus

6 Hypothalamus - Mammillary bodies

7 Amygdala

8 Thalamus + subthalamic

9a Hippocampus anterior

9b Hippocampus posterior

10 Temporal cortex

11 Precentral gyrus - Motor cortex

12a Primary visual cortex anterior

12b Primary visual cortex posterior

13 Parietal lobule

14 Cerebellum

15 Midbrain - Substantia nigra

16 Rostral pons with locus coeruleus - Basis pontis

17 Medulla with dorsal efferent nuleus of vagus Inferior olive

18 Spinal cord at 3 levels

19 Optic chiasm

20 White matter lesion

21 White matter lesion

22 White matter lesion

23 White matter lesion

Appendix III

Clinical details of MS cases used in this project											Cases/blocks used in each study						
Case	Region	Age	Gender	Brain weight (g)	PMI (hours)	CSF pH	Cause of death	MS classification	Snap frozen	FFPE	Astrocyte phenotype study (Chapter 2)	LCM study (Chapter 3)	Microarray study (Chapter 4)	Validation IHC (Chapter 5)	Validation qPCR (Chapter 5)	Validation WB (Chapter 5)	Validation MALDI-MS (Chapter 5)
MS50	P1E4	72	F	1175	8	-	Bronchpneumonia, multiple sclerosis	SPMS	P1E4			P1E4	P1E4				
MS57	P1A6 P1C2 A2D5 P1B5	77	F	1000	9	6.62	General deterioration, lung infection, treatment witheld	SPMS	P1A6 P1C2 A2D5 P1B5			P1A6	P1A6				
MS67	P2C7	86	F	1101	11	6.57	Bronchopneumonia	SPMS	P2C7			P2C7	P2C7				
MS71	P2C3 P2C2	78	F	1062	5	7.15	Metastatic carcinoma of bronchus	SPMS	P2C3 P2C2			P2C3	P2C3				
MS93	A1C3 P3B6	57	F	930	25	-	Aspiration pneumonia, multiple sclerosis	SPMS	A1C3 P3B6								
MS100	P2B3	46	M	1409	7	-	Pneumonia	SPMS	P2B3			P2B3	P2B3				
MS103	P1D3 P1B3 A3B4	77	F	1183	7	-	Pneumonia	SPMS	P1D3 P1B3 A3B4					A3B4	A3B4	A3B4	A3B4
MS105	A4B2	73	M	1156	8	6.47	Pneumonia, infection	SPMS	A4B2					A4B2	A4B2	A4B2	A4B2
MS106	P5B1	39	F	1010	18	6.48	Bronchopneumonia	-	P5B1					P5B1	P5B1	P5B1	P5B1
MS107	P4C3	38	M	1273	19	6.90	Aspiration pneumonia, pulmonary oedema	RPMS	P4C3					P4C3	P4C3	P4C3	P4C3
MS159	P1B2	55	F	1000	24	7.10	Amitriptyline overdose	SPMS	P1B2								
MS200	1 12 21 P1D2	44	F	1205	20	6.90	Urinary tact infection, sepsis, multiple sclerosis	SPMS	P1D2	1 12 21	1 12 21			P1D2	P1D2		
MS235	10 12 21 P3D2	53	M	933	14	6.90	Septicaemia due to urinary tract infection, multiple sclerosis	SPMS	P3D2	10 12 21	10 12 21			P3D2	P3D2	P3D2	P3D2
MS237	1 12 21	77	M	1190	19	6.80	Pneumonia, heart attack	SPMS		1 12 21	1 12 21						
MS241	1 12 21	83	F	1204	15	6.70	septicaemia, bronchopneumonia, multiple sclerosis, type 2 diabetes	SPMS		1 12 21	1 12 21						
MS242	1 11 12	57	F	931	12	6.30	Sepsis	SPMS		1 11 12	1 11 12						
MS245	1 8 12	64	M	1120	25	6.90	Bronchopneumonia, multiple sclerosis	SPMS		1 8 12	1 8 12						
MS249	1 12 13	59	F	885	8	6.70	Chest infection, heart failure	RRMS		1 12 13	1 12 13						
MS296	1 20 22	59	M	1315	22	6.70	Multiple sclerosis	SPMS		1 20 22	1 20 22						
MS298	9 19 20	72	M	932	11	-	Chest infection, multiple sclerosis	SPMS		9 19 20	9 19 20						
MS300	10 12 23	56	F	1090	13	7.70	Sepsis, urinary tract infection caused by multiple sclerosis	SPMS		10 12 23	10 12 23						
MS303	12 19 20	63	F	1125	24	7.10	Acute pulmonary oedema, urinary tract infection, acute renal impairment, multiple sclerosis, ischaemic heart disease, hypertension, pneumonia	SPMS		12 19 20	12 19 20						
MS307	12 19 20	55	M	1215	19	7.00	Multiple sclerosis	SPMS		12 19 20	12 19 20						

Clinical details of MS cases included in the different studies of this project

The cases used in chapter 2, the astrocyte phenotype study (grey), chapter 3, the LCM study (blue), chapter 4, the microarray study (peach) and chapter 5, the validation cases (yellow). All remaining snap frozen MS brain blocks documented in this table failed to follow quality control (QC) for NAWM tissue and therefore were not used throughout the project.

Appendix III cont.

Clinical details of control cases used in this project											Cases/blocks used in each study						
Case	Region	Age	Gender	Brain weight (g)	PMI (hours)	CSF pH	Cause of death	MS classification	Snap Frozen	FFPE	Astrocyte phenotype study (Chapter 2)	LCM study (Chapter 3)	Microarray study (Chapter 4)	Validation IHC (Chapter 5)	Validation qPCR (Chapter 5)	Validation WB (Chapter 5)	Validation MALDI-MS (Chapter 5)
CO14	P2A2 P2C2	64	M	1431	18	-	Cardiac failure	N/A	P2A2 P2C2					P2C2	P2C2	P2C2	P2C2
CO15	PAR PFC	82	M	1166	21	-	Unknown	N/A		PAR PFC	PAR PFC						
CO22	P1C2 P1C3	69	F	1130	33	7.80	Lung cancer	N/A	P1C2 P1C3				P1C2	P1C2	P1C2		
CO25	10 P1B2 P3C2 P2A3	35	M	1670	22	-	Carcinoma of the tongue	N/A	P1B2 P3C2 P2A3	10	10		P2A3	P1B1	P1B1	P1B1	P1B1
CO26	P1B1 P1A2	78	F	1250	33	6.70	Myeloid leukemia	N/A	P1B1 P1A2					P1B1	P1B1	P1B1	P1B1
CO28	A2D2	60	F	1132	13	-	Ovarian cancer	N/A	A2D2								
CO30	P2A2	75	M	1256	17	6.60	cva, aspiration pneumonia	N/A	P2A2				P2A2				
CO32	1 10	88	M	1233	22	6.50	Prostate cancer, bone metastases	N/A		1 10	1 10						
CO36	1 10	68	M	1394	30	7.70	Coronary pulmonale heart failure, fibrosing alveolitis, coronary artery artheroma	N/A		1 10	1 10						
CO37	1 10	84	M	1100	5	-	Bladder cancer, pneumonia	N/A		1 10	1 10						
PDCO01	P2E4	76	M	1456	24	-	Acute on chronic myocardial ischaemia	N/A	P2E4					P2E4	P2E4	P2E4	P2E4
PDCO03	1 4	84	M	1257	49	-	Pancreatic carcinoma & Gastrointestinal Haemorrhage	N/A		1 4	1 4						
PDCO11	1 4	71	M	1443	52	-	Haemopericardium, ruptured acute myocardial infarction	N/A		1 4	1 4						
PDCO16	1 4 P1B1	91	F	1090	22	-	Bronchial pneumonia, old age	N/A	P1B1	1 4	1 4		P1B1				
PDCO22	1 11 P2B1	65	M	1090	12	7.70	Malignant squamous cell carcinoma of the lung	N/A	P2B1	1 11	1 11			P2B1	P2B1	P2B1	P2B1
PDCO23	P1B1 P2B4	78	F	1418	23	-	Unknown	N/A	P1B1 P2B4				P2B4				
07/085*	-	101	F	-	18	5.90	Bronchpneumonia	N/A				07/085					

Clinical details of control cases included in the different studies of this project

The cases used in chapter 2, the astrocyte phenotype study (grey), chapter 3, the LCM study (blue), chapter 4, the microarray study (peach) and chapter 5, the validation cases (yellow). All remaining snap frozen control brain blocks documented in the table failed to follow QC for control tissue and therefore were not used throughout the project.

07/085* case supplied by the Sheffield Brain Tissue Bank and used only in chapter 3 as the tissue block failed the QC for control tissue for the proceeding studies.

Appendix IV

Laboratory recipes

Histology solution and reagents

LFB
0.1% LFB - 0.5g Luxol fast blue powder was diluted in 500ml 95% ethanol (Fischer, UK) and 2.5 ml of glacial acetic acid added.

0.05% Lithium carbonate - 0.25g lithium carbonate was dissolved in 500ml of d. H_2O

TBS (1x)
6.05g (50mM) Tris buffer (Fisher Scientific, Loughborough, UK) and 8.76g (150mM) Sodium chloride (Merck,) was made up to 1L in d.H_2O, pH to 7.6.

Acid/Alcohol
20ml concentrate hydrochloric acid was diluted in 1780ml 70% ethanol

Scott's Tap water
8.75g sodium bicarbonate and 50.0g magnesium sulphate were dissolved in 2.5L water

EDTA 1mM (antigen retrieval)
0.15g Ethylenediaminetetraacetic acid (EDTA) was diluted in 500 ml d.H_2O pH to 8.0

TSC (antigen retrieval)
1.5g tri-sodium citrate (TSC) was diluted in 500 ml d.H_2O pH to 6.5

Protein extraction from PM CNS tissue

Suspension buffer
10mM Tris-Hcl pH7.4, 0.8M NaCl, 1mM ethylene glycol tetraacetic acid (EGTA), 10% sucrose, 0.1mM phenylmethylsulfonyl fluoride (PMSF)

Extraction buffer
10 ml suspension buffer + 1x cOmplete, mini, EDTA-free protease inhibitor cocktail tablet (Roche Applied Sciences, UK)

Commercial protein extraction buffer
CelLytic MT Cell Lysis Reagent (Sigma, UK) + protease inhibitor cocktain (Sigma, UK) 1:10 ratio

Agarose gel buffer/running buffer

Tris-acetate-EDTA (TAE) (1x)
40mM Tris base (Sigma, UK), 20mM acetic acid (Fisher Scientific, UK), 1mM EDTA (Sigma, UK) pH 8.0

WB buffers and reagents

TBS-Tween (TBST)
0.05% - 0.5ml Tween 20 dissolved in in 1L TBS

Polyacrylamide precast gels
Novex® 18% Tris-Glycine Mini Gels, 1.0 mm, 10 well/12 well (Life technologies, UK)

Laemmli sample buffer (6x) – reagents from Fisher Scientific, UK

2.4ml 0.5M Tris, pH 6.8
2.4g SDS
9.4ml glycerol
24mg bromophenol blue
1.86g DTT
4.2ml d.H_20 (to make up to 20ml total)

Novex Sample buffer (2x)
Novex Tris-Glycine SDS sample buffer (2x), (Life technologies, UK)

Reducing agent
NuPAGE Sample Reducing Agent (10X) (Life technologies, UK)

Protein molecular weight marker
Precision plus protein dual colour extra standard (Bio-Rad, UK)

Running buffer
(10x) Novex Tris-Glycine running buffer (Life technologies, UK) 100ml (10x) was diluted in 900ml d.H_2O

Transfer Buffer
(25x) Novex Tris-Glycine transfer buffer (Life technologies, UK) 40ml (25x) was diluted in 960 ml d.H_2O

5% Blocking buffer
5g blotting grade blocker (Biorad, UK) dissolved in 100ml TBST

Appendix V

Differentially expressed genes in astrocytes isolated from MS NAWM in comparison to Control WM identified by DAVID analysis

These tables represent the functional groups of genes identified in the isolated astrocytes which were classified as up-regulated or down-regulated in the NAWM in comparison to astrocytes isolated from the control WM.

Immune response

Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
209933_s_at	0.0433	up	1.51	CD300A	CD300a molecule
206508_at	0.0474	up	1.61	CD70	CD70 molecule
209619_at	0.0075	up	2.73	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
218002_s_at	0.0237	down	-1.94	CXCL14	chemokine (C-X-C motif) ligand 14
222484_s_at	0.0059	down	-2.55	CXCL14	chemokine (C-X-C motif) ligand 14
225353_s_at	0.0164	up	1.77	C1QC	complement component 1, q subcomponent, C chain
217767_at	0.0352	up	1.94	C3	complement component 3
214022_s_at	0.0306	up	1.79	IFITM1	interferon induced transmembrane protein 1 (9-27)
201315_x_at	0.0460	up	1.76	IFITM2	interferon induced transmembrane protein 2 (1-8D)
224079_at	0.0393	up	1.54	IL17C	interleukin 17C
203233_at	0.0130	up	1.54	IL4R	interleukin 4 receptor

211990_at	0.0026	up	2.01	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
201137_s_at	0.0056	up	1.85	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
204748_at	0.0205	down	-1.56	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
211921_x_at	0.0482	up	1.64	PTMA	prothymosin, alpha
200772_x_at	0.0408	up	1.70	PTMA	prothymosin, alpha
201331_s_at	0.0360	down	-1.73	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced
204158_s_at	0.0304	up	1.66	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3
204787_at	0.0488	up	1.51	VSIG4	V-set and immunoglobulin domain containing 4

Homeostasis

Metal ion binding/iron					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
212788_x_at	0.0304	up	2.24	FTL	ferritin, light polypeptide
211456_x_at	0.0435	up	2.22	MT1P2	metallothionein 1 pseudogene 2

204745_x_at	0.0313	up	2.26	MT1G	metallothionein 1G
208581_x_at	0.0416	up	2.23	MT1X	metallothionein 1X
212185_x_at	0.0318	up	2.52	MT2A	metallothionein 2A
205970_at	0.0157	up	2.02	MT3	metallothionein 3
222258_s_at	0.0417	up	2.01	SH3BP4	SH3-domain binding protein 4
215008_at	0.0093	down	-1.57	TLL2	tolloid-like 2
214064_at	0.0478	up	2.21	TF	transferrin

Neurotrophic support					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
206527_at	0.0167	up	1.94	ABAT	4-aminobutyrate aminotransferase
1554816_at	0.0323	up	1.56	ASTN2	astrotactin 2
204995_at	0.0234	down	-1.78	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
202428_x_at	0.0176	up	1.85	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
209389_x_at	0.0214	up	1.84	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
211070_x_at	0.0142	up	1.80	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)

215000_s_at	0.0343	down	-1.66	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)
1557122_s_at	0.0453	down	-1.87	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
226271_at	0.0085	down	-1.59	GDAP1	ganglioside-induced differentiation-associated protein 1
232193_at	0.0188	down	-1.68	GSTT1	Glutathione S-transferase theta 1
218152_at	0.0081	down	-1.53	HMG20A	high-mobility group 20A
229463_at	0.0101	down	-3.11	NTRK2	neurotrophic tyrosine kinase, receptor, type 2
202165_at	0.0468	down	-1.82	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2
1558295_a_at	0.0489	down	-1.62	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2
232073_at	0.0275	down	-1.74	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2
203431_s_at	0.0363	down	-1.96	RICS	Rho GTPase-activating protein
242196_at	0.0098	down	-1.81	RICS	Rho GTPase-activating protein
229648_at	0.0071	down	-2.08	RICS	Rho GTPase-activating protein
240425_x_at	0.0412	down	-1.66	ROBO2	Roundabout, axon guidance receptor, homolog 2 (Drosophila)

214930_at	0.0381	down	-1.92	SLITRK5	SLIT and NTRK-like family, member 5
209747_at	0.0235	up	1.55	TGFB3	transforming growth factor, beta 3

Transcription					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
203744_at	0.0152	down	-1.58	HMGB3	high-mobility group box 3
219269_at	0.0078	up	1.67	HMBOX1	homeobox containing 1
213931_at	0.0159	down	-2.24	ID2 /// ID2B	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)
223492_s_at	0.0281	down	-1.87	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1
228012_at	0.0423	down	-1.77	MATR3	matrin 3
221690_s_at	0.0083	down	-1.56	NLRP2	NLR family, pyrin domain containing 2
202599_s_at	0.0318	down	-1.91	NRIP1	nuclear receptor interacting protein 1
222605_at	0.0314	down	-1.69	RCOR3	REST corepressor 3
204530_s_at	0.0354	down	-1.57	TOX	thymocyte selection-associated high mobility group box
208986_at	0.0341	up	1.60	TCF12	transcription factor 12
50221_at	0.0204	up	1.53	TFEB	transcription factor EB

212435_at	0.0077	down	-1.73	TRIM33	tripartite motif-containing 33
233245_at	0.0304	up	1.53	UHRF1BP1	UHRF1 binding protein 1
1557260_a_at	0.0108	down	-1.55	ZNF382	zinc finger protein 382
231940_at	0.0397	down	-1.52	ZNF529	zinc finger protein 529
225266_at	0.0154	up	1.71	ZNF652	zinc finger protein 652
1570366_x_at	0.0430	up	1.53	ZNF709	zinc finger protein 709
228988_at	0.0417	down	-1.62	ZNF711	zinc finger protein 711
218919_at	0.0069	down	-1.53	ZFAND1	zinc finger, AN1-type domain 1
228749_at	0.0273	down	-1.58	ZDBF2	zinc finger, DBF-type containing 2
229240_at	0.0165	down	-1.67	ZDHHC21	Zinc finger, DHHC-type containing 21

Cell signaling/communication and transport

MAPK Signaling pathway					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
211535_s_at	0.0039	up	1.63	FGFR1	fibroblast growth factor receptor 1
218181_s_at	0.0160	up	1.54	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
201460_at	0.0387	up	1.70	MAPKAPK 2	mitogen-activated protein kinase-activated protein kinase 2
204061_at	0.0324	up	1.63	PRKX	protein kinase, X-linked
Insulin Signaling pathway					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title

211959_at	0.0242	up	2.24	IGFBP5	insulin-like growth factor binding protein 5
203424_s_at	0.0096	up	1.71	IGFBP5	insulin-like growth factor binding protein 5
Calcium signal					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
209281_s_at	0.0488	down	-1.58	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1
235781_at	0.0389	down	-1.68	CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit
211985_s_at	0.0399	down	-1.91	CALM1	calmodulin 1 (phosphorylase kinase, delta)
227259_at	0.0358	down	-1.72	CD47	CD47 molecule
203798_s_at	0.0445	down	-3.31	VSNL1	visinin-like 1
Ubiquitin					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
202203_s_at	0.0131	down	-1.51	AMFR	autocrine motility factor receptor
202984_s_at	0.0368	down	-1.53	BAG5	BCL2-associated athanogene 5
218751_s_at	0.0405	down	-2.21	FBXW7	F-box and WD repeat domain containing 7
224802_at	0.0334	down	-1.81	NDFIP2	Nedd4 family interacting protein 2
202268_s_at	0.0387	down	-1.64	NAE1	NEDD8 activating enzyme E1 subunit 1
227040_at	0.0083	down	-1.52	NHLRC3	NHL repeat containing 3

203871_at	0.0007	down	-1.63	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3
237439_at	0.0118	down	-1.71	USP43	ubiquitin specific peptidase 43
Apoptosis/cell death					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
203685_at	0.0468	up	1.76	BCL2	B-cell CLL/lymphoma 2
225097_at	0.0282	up	2.43	HIPK2	homeodomain interacting protein kinase 2
225368_at	0.0345	up	2.63	HIPK2	homeodomain interacting protein kinase 2
225115_at	0.0397	up	1.83	HIPK2	homeodomain interacting protein kinase 2
204037_at	0.0183	up	2.39	LPAR1	lysophosphatidic acid receptor 1
200788_s_at	0.0221	up	1.53	PEA15	phosphoprotein enriched in astrocytes 15
227751_at	0.0377	down	-1.75	PDCD5	programmed cell death 5
Cell junction/synapses					
Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
1557122_s_at	0.0453	down	-1.87	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
230644_at	0.0436	down	-1.98	LRFN5	leucine rich repeat and fibronectin type III domain containing 5

213325_at	0.0489	down	-1.56	PVRL3	poliovirus receptor-related 3
220460_at	0.0113	down	-1.63	SLCO1C1	solute carrier organic anion transporter family, member 1C1
216086_at	0.0383	down	-2.47	SV2C	synaptic vesicle glycoprotein 2C
202507_s_at	0.0225	down	-1.58	SNAP25	synaptosomal-associated protein, 25kDa
203016_s_at	0.0407	down	-1.85	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein
203019_x_at	0.0486	down	-1.88	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein
207100_s_at	0.0444	down	-1.93	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)
213480_at	0.0386	down	-1.57	VAMP4	vesicle-associated membrane protein 4

Cell signaling/communication and transport (cont.)

Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
214151_s_at	0.0203	down	-1.58	CCPG1	cell cycle progression 1
214152_at	0.0358	down	-1.57	CCPG1	cell cycle progression 1
222156_x_at	0.0423	down	-1.59	CCPG1	cell cycle progression 1
219707_at	0.0409	up	1.57	CPNE7	copine VII
215151_at	0.0049	up	1.52	DOCK10	dedicator of cytokinesis 10
209343_at	0.0286	up	2.57	EFHD1	EF-hand domain family, member D1

205117_at	0.0101	up	2.25	FGF1	fibroblast growth factor 1 (acidic)
224761_at	0.0205	up	1.50	GNA13	guanine nucleotide binding protein (G protein), alpha 13
223434_at	0.0012	up	1.60	GBP3	guanylate binding protein 3
201631_s_at	0.0489	up	1.52	IER3	immediate early response 3
231179_at	0.0295	up	1.60	IP6K3	inositol hexakisphosphate kinase 3
37796_at	0.0112	up	1.83	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4
227357_at	0.0430	down	-1.73	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3
212530_at	0.0283	up	1.81	NEK7	NIMA (never in mitosis gene a)-related kinase 7
219489_s_at	0.0247	up	1.63	NXN	nucleoredoxin
212183_at	0.0460	down	-1.55	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4
212719_at	0.0339	up	1.56	PHLPP	PH domain and leucine rich repeat protein phosphatase
223207_x_at	0.0164	up	1.57	PHPT1	phosphohistidine phosphatase 1
212239_at	0.0410	down	-1.73	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
210183_x_at	0.0167	up	1.53	PNN	pinin, desmosome associated protein

208479_at	0.0497	down	-1.78	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
227892_at	0.0422	down	-1.62	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit
200605_s_at	0.0472	down	-1.76	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
225207_at	0.0390	up	2.35	PDK4	pyruvate dehydrogenase kinase, isozyme 4
202252_at	0.0215	up	1.94	RAB13	RAB13, member RAS oncogene family
219202_at	0.0389	up	1.89	RHBDF2	rhomboid 5 homolog 2 (Drosophila)
205334_at	0.0190	up	1.81	S100A1	S100 calcium binding protein A1
219911_s_at	0.0141	up	1.76	LOC100134295 /// SLCO4A1	similar to Solute carrier organic anion transporter family, member 4A1 /// solute carrier organic anion transporter family, member 4A1
207057_at	0.0057	down	-1.75	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
226931_at	0.0092	up	1.55	TMTC1	transmembrane and tetratricopeptide repeat containing 1
204122_at	0.0476	up	1.54	TYROBP	TYRO protein tyrosine kinase binding protein

1565783_at	0.0479	up	1.62	TNK2	tyrosine kinase, non-receptor, 2
202933_s_at	0.0295	up	1.62	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1

Cytoskeleton and cell growth

Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
225112_at	0.0315	down	-1.58	ABI2	abl interactor 2
209028_s_at	0.0433	down	-1.59	ABI1	abl-interactor 1
201305_x_at	0.0134	up	1.93	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
201306_s_at	0.0161	up	1.82	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
203862_s_at	0.0476	down	-1.73	ACTN2	actinin, alpha 2
227064_at	0.0233	up	1.53	ANKRD40	ankyrin repeat domain 40
235848_x_at	0.0467	down	-1.56	ATL2	Atlastin GTPase 2
203590_at	0.0159	up	1.50	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2
203762_s_at	0.0349	down	-1.83	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1
203763_at	0.0344	down	-1.99	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1
223319_at	0.0219	down	-1.56	GPHN	gephyrin
209721_s_at	0.0223	down	-1.65	IFFO1	intermediate filament family orphan 1

36030_at	0.0205	down	-1.61	IFFO1	intermediate filament family orphan 1
209898_x_at	0.0266	down	-1.56	ITSN2	intersectin 2
209244_s_at	0.0053	up	1.80	KIF1C	kinesin family member 1C
219573_at	0.0308	down	-1.56	LRRC16A	leucine rich repeat containing 16A
204692_at	0.0259	up	1.69	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4
212567_s_at	0.0191	up	2.05	MAP4	microtubule-associated protein 4
212566_at	0.0087	up	2.14	MAP4	microtubule-associated protein 4
200835_s_at	0.0198	up	1.62	MAP4	microtubule-associated protein 4
33850_at	0.0409	up	1.83	MAP4	microtubule-associated protein 4
243_g_at	0.0294	up	1.73	MAP4	microtubule-associated protein 4
218251_at	0.0113	up	2.16	MID1IP1	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))
228905_at	0.0052	down	-1.62	PCM1	pericentriolar material 1
235127_at	0.0128	up	1.89	PMP2	peripheral myelin protein 2
206826_at	0.0179	up	2.04	PMP2	peripheral myelin protein 2
201928_at	0.0268	up	1.72	PKP4	plakophilin 4
212397_at	0.0432	up	1.69	RDX	radixin
230355_at	0.0181	down	-1.52	SEPT13	septin 13

209000_s_at	0.0372	up	2.18	SEPT8	septin 8
209447_at	0.0122	down	-1.66	SYNE1	spectrin repeat containing, nuclear envelope 1
225485_at	0.0389	down	-1.74	TSGA14	testis specific, 14
204165_at	0.0387	down	-2.39	WASF1	WAS protein family, member 1

RNA/DNA processing

Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
209903_s_at	0.0339	down	-1.64	ATR	ataxia telangiectasia and Rad3 related
201101_s_at	0.0192	down	-1.59	BCLAF1	BCL2-associated transcription factor 1
200810_s_at	0.0483	down	-1.97	CIRBP	cold inducible RNA binding protein
1562830_at	0.0405	up	1.63	METT5D1	methyltransferase 5 domain containing 1
225761_at	0.0066	down	-1.52	PAPD4	PAP associated domain containing 4
213677_s_at	0.0482	down	-1.55	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
221868_at	0.0436	up	1.93	PAIP2B	poly(A) binding protein interacting protein 2B
226453_at	0.0190	up	1.51	RNASEH2C	ribonuclease H2, subunit C
208319_s_at	0.0181	down	-1.61	RBM3	RNA binding motif (RNP1, RRM) protein 3
212028_at	0.0401	down	-1.58	RBM25	RNA binding motif protein 25

212030_at	0.0144	down	-1.60	RBM25	RNA binding motif protein 25
224623_at	0.0386	down	-1.75	LOC728554 /// THOC3	similar to THO complex 3 /// THO complex 3
206055_s_at	0.0392	down	-1.61	SNRPA1	small nuclear ribonucleoprotein polypeptide A'
1559545_at	0.0420	down	-1.68	SNRPN	small nuclear ribonucleoprotein polypeptide N
201589_at	0.0259	up	1.73	SMC1A	structural maintenance of chromosomes 1A
212894_at	0.0207	down	-1.55	SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)
217834_s_at	0.0306	up	1.55	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
217833_at	0.0387	down	-1.56	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein

Protein metabolism

Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
226609_at	0.0112	down	-1.82	DCBLD1	discoidin, CUB and LCCL domain containing 1
225174_at	0.0302	down	-1.65	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10
213271_s_at	0.0134	down	-1.87	DOPEY1	dopey family member 1
40612_at	0.0327	down	-1.65	DOPEY1	dopey family member 1
203113_s_at	0.0058	up	1.53	EEF1D	eukaryotic translation elongation factor 1 delta (guanine

					nucleotide exchange protein)
214394_x_at	0.0414	up	1.52	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
211345_x_at	0.0198	up	1.54	EEF1G	eukaryotic translation elongation factor 1 gamma
215554_at	0.0174	down	-1.84	GPLD1	glycosylphosphatidylinositol specific phospholipase D1
208798_x_at	0.0114	down	-2.53	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A
213650_at	0.0239	down	-1.99	GOLGA8A /// GOLGA8B	golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B
210425_x_at	0.0113	down	-2.41	GOLGA8B	golgi autoantigen, golgin subfamily a, 8B
222149_x_at	0.0112	down	-1.80	GOLGA8C /// GOLGA8D /// GOLGA8E /// GOLGA8F /// GOLGA8G	golgi autoantigen, golgin subfamily a, 8C /// golgi autoantigen, golgin subfamily a, 8D /// golgi autoantigen, golgin subfamily a, 8E /// golgi autoantigen, golgin subfamily a, 8F /// golgi autoantigen, golgin subfamily a, 8G
213737_x_at	0.0276	down	-1.72	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene
213212_x_at	0.0142	down	-1.63	FLJ40113 /// LOC440295	golgi autoantigen, golgin subfamily a-like pseudogene /// hypothetical protein LOC440295

207783_x_at	0.0159	up	1.63	HUWE1	HECT, UBA and WWE domain containing 1
203518_at	0.0072	down	-1.51	LYST	lysosomal trafficking regulator
238530_at	0.0364	down	-1.64	NNT	nicotinamide nucleotide transhydrogenase
217863_at	0.0068	down	-1.54	PIAS1	protein inhibitor of activated STAT, 1
208616_s_at	0.0325	up	1.59	PTP4A2	protein tyrosine phosphatase type IVA, member 2
208732_at	0.0326	down	-1.99	RAB2A	RAB2A, member RAS oncogene family
208733_at	0.0032	down	-1.92	RAB2A	RAB2A, member RAS oncogene family
208929_x_at	0.0026	up	1.82	RPL13	ribosomal protein L13
212191_x_at	0.0103	up	1.91	RPL13	ribosomal protein L13
212933_x_at	0.0054	up	1.60	RPL13	ribosomal protein L13
212734_x_at	0.0023	up	1.95	RPL13	ribosomal protein L13
214351_x_at	0.0011	up	1.89	RPL13	ribosomal protein L13
200716_x_at	0.0024	up	1.53	RPL13A	ribosomal protein L13a
212790_x_at	0.0008	up	1.61	RPL13A	ribosomal protein L13a
210646_x_at	0.0007	up	1.59	RPL13A	ribosomal protein L13a
211942_x_at	0.0026	up	1.73	RPL13A /// RPL13AP25 /// RPL13AP5 /// RPL13AP6	ribosomal protein L13a /// ribosomal protein L13a pseudogene 25 /// ribosomal protein L13a pseudogene 5 /// ribosomal protein L13a pseudogene 6
200869_at	0.0141	up	1.68	RPL18A /// RPL18AP3	ribosomal protein L18a /// ribosomal protein L18a pseudogene 3

200003_s_at	0.0158	up	1.56	RPL28	ribosomal protein L28
200062_s_at	0.0014	up	1.71	RPL30	ribosomal protein L30
200092_s_at	0.0029	up	1.63	RPL37	ribosomal protein L37
201429_s_at	0.0011	up	1.67	RPL37A	ribosomal protein L37a
200936_at	0.0102	up	1.54	RPL8	ribosomal protein L8
200095_x_at	0.0056	up	1.55	RPS10	ribosomal protein S10
211542_x_at	0.0096	up	1.52	RPS10	ribosomal protein S10
200031_s_at	0.0008	up	1.55	RPS11	ribosomal protein S11
200819_s_at	0.0018	up	1.51	RPS15	ribosomal protein S15
226131_s_at	0.0029	up	1.52	RPS16	ribosomal protein S16
201049_s_at	0.0215	up	1.52	RPS18	ribosomal protein S18
202649_x_at	0.0032	up	1.75	RPS19	ribosomal protein S19
213414_s_at	0.0046	up	1.97	RPS19	ribosomal protein S19
212433_x_at	0.0018	up	1.55	RPS2	ribosomal protein S2
203107_x_at	0.0039	up	1.50	RPS2	ribosomal protein S2
200949_x_at	0.0024	up	1.58	RPS20	ribosomal protein S20
200834_s_at	0.0307	up	1.57	RPS21	ribosomal protein S21
208904_s_at	0.0013	up	1.53	RPS28	ribosomal protein S28
200024_at	0.0225	up	1.53	RPS5	ribosomal protein S5
214317_x_at	0.0140	up	1.59	RPS9	ribosomal protein S9
200763_s_at	0.0145	up	1.80	RPLP1	ribosomal protein, large, P1
225302_at	0.0491	down	-1.56	TMX3	thioredoxin-related transmembrane protein 3
201042_at	0.0029	up	1.59	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)

214785_at	0.0189	down	-1.78	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)
202172_at	0.0208	up	1.54	VEZF1	vascular endothelial zinc finger 1
202173_s_at	0.0338	up	1.52	VEZF1	vascular endothelial zinc finger 1

Miscellaneous

Probe Set ID	p-value	Regulation	Fold change	Gene Symbol	Gene Title
226969_at	0.0300	down	-1.61	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase
244699_at	0.0170	down	-2.49	AHI1	Abelson helper integration site 1
226665_at	0.0118	down	-1.60	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
203180_at	0.0153	down	-1.53	ALDH1A3	aldehyde dehydrogenase 1 family, member A3
203566_s_at	0.0204	down	-1.67	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase
220076_at	0.0356	down	-1.61	ANKH	ankylosis, progressive homolog (mouse)
221850_x_at	0.0234	down	-1.54	AGAP11 /// AGAP4 /// AGAP6 /// AGAP7 /// AGAP8	ankyrin repeat and GTPase domain Arf GTPase activating protein 11 /// ArfGAP with GTPase domain, ankyrin repeat and PH domain 4 /// ArfGAP with GTPase domain, ankyrin repeat and PH

					domain 6 /// ArfGAP with GTPase domain, ankyrin repeat and PH domain 7 /// ArfGAP with GTPase domain, ankyrin repeat and PH domain 8
225731_at	0.0416	down	-1.69	ANKRD50	ankyrin repeat domain 50
204416_x_at	0.0131	up	1.84	APOC1	apolipoprotein C-I
219335_at	0.0413	down	-1.68	ARMCX5	armadillo repeat containing, X-linked 5
226055_at	0.0291	up	1.55	ARRDC2	arrestin domain containing 2
1553422_s_at	0.0137	down	-1.56	A2BP1	ataxin 2-binding protein 1
203795_s_at	0.0231	down	-1.51	BCL7A	B-cell CLL/lymphoma 7A
219966_x_at	0.0452	up	1.54	BANP	BTG3 associated nuclear protein
229985_at	0.0480	up	1.83	BTNL9	Butyrophilin-like 9
209301_at	0.0494	up	1.66	CA2	carbonic anhydrase II
205199_at	0.0372	up	1.53	CA9	carbonic anhydrase IX
209763_at	0.0488	down	-1.55	CHRDL1	chordin-like 1
244165_at	0.0185	down	-1.71	C10orf18	chromosome 10 open reading frame 18
226487_at	0.0439	up	1.51	C12orf34	chromosome 12 open reading frame 34
225087_at	0.0039	down	-1.60	C16orf63	chromosome 16 open reading frame 63
213237_at	0.0287	up	1.54	C16orf88	chromosome 16 open reading frame 88
226901_at	0.0177	down	-1.52	C17orf58	chromosome 17 open reading frame 58

214696_at	0.0224	down	-1.82	C17orf91	chromosome 17 open reading frame 91
228106_at	0.0367	down	-1.54	C4orf30	chromosome 4 open reading frame 30
230424_at	0.0207	down	-1.82	C5orf13	chromosome 5 open reading frame 13
226018_at	0.0208	up	1.57	C7orf41	chromosome 7 open reading frame 41
204363_at	0.0399	down	-2.15	F3	coagulation factor III (thromboplastin, tissue factor)
220175_s_at	0.0115	down	-1.98	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6 /// CBWD7	COBW domain containing 1 /// COBW domain containing 2 /// COBW domain containing 3 /// COBW domain containing 5 /// COBW domain containing 6 /// COBW domain containing 7
208896_at	0.0342	down	-1.52	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
222721_at	0.0192	up	1.51	DOCK5	Dedicator of cytokinesis 5
202673_at	0.0446	down	-1.61	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
230158_at	0.0467	down	-1.57	DPY19L2	dpy-19-like 2 (C. elegans)
244142_at	0.0293	down	-2.01	DTNA	dystrobrevin, alpha
230496_at	0.0436	up	1.78	FAM123A	family with sequence similarity 123A
233974_s_at	0.0376	up	1.50	FAM129B	family with sequence similarity 129, member B

225667_s_at	0.0446	down	-2.05	FAM84A	family with sequence similarity 84, member A
225864_at	0.0246	up	1.67	FAM84B	family with sequence similarity 84, member B
219200_at	0.0474	down	-1.62	FASTKD3	FAST kinase domains 3
219429_at	0.0484	up	2.09	FA2H	fatty acid 2-hydroxylase
200019_s_at	0.0049	up	1.57	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed
223618_at	0.0170	down	-1.53	FMN2	formin 2
229007_at	0.0039	down	-1.56	LOC283788	FSHD region gene 1 pseudogene
1553971_a_at	0.0005	up	1.59	GATS	GATS, stromal antigen 3 opposite strand
236924_at	0.0196	down	-1.71	GLMN	Glomulin, FKBP associated protein
217414_x_at	0.0479	up	1.89	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2
217756_x_at	0.0086	up	1.60	HYPK /// SERF2	Huntingtin interacting protein K /// small EDRK-rich factor 2
224625_x_at	0.0255	up	1.60	HYPK /// SERF2	Huntingtin interacting protein K /// small EDRK-rich factor 2
242822_at	0.0496	up	1.79	MGC39584	Hypothetical gene supported by BC029568
1559650_at	0.0358	down	-1.53	LOC100128081	Hypothetical LOC100128081
235174_s_at	0.0165	down	-1.57	LOC100128822	hypothetical LOC100128822

230526_at	0.0323	up	1.67	LOC100131096	hypothetical LOC100131096
230495_at	0.0314	down	-1.68	LOC150568	hypothetical LOC150568
1559489_a_at	0.0360	up	1.79	LOC257358	hypothetical LOC257358
229623_at	0.0374	down	-1.76	FLJ12993	Hypothetical LOC441027
233610_at	0.0008	down	-1.56	LOC645355	hypothetical LOC645355
226419_s_at	0.0332	down	-1.60	FLJ44342	hypothetical LOC645460
229546_at	0.0311	down	-1.98	LOC653602	hypothetical LOC653602
227183_at	0.0376	up	1.55	LOC728264	hypothetical LOC728264
229715_at	0.0352	down	-1.61	DKFZp686O24166	hypothetical protein DKFZp686O24166
224835_at	0.0101	down	-2.04	RP5-1022P6.2	hypothetical protein KIAA1434
1564490_at	0.0469	up	1.80	LOC100128830	hypothetical protein LOC100128830
230653_at	0.0195	up	1.62	LOC100132218 /// LOC728555	hypothetical protein LOC100132218 /// hypothetical LOC728555
1562754_at	0.0426	up	1.68	LOC339260	hypothetical protein LOC339260
1558404_at	0.0486	down	-1.76	LOC644242	Hypothetical protein LOC644242
230454_at	0.0347	down	-1.72	ICA1L	islet cell autoantigen 1,69kDa-like
228793_at	0.0231	down	-1.63	JMJD1C	jumonji domain containing 1C

213752_at	0.0045	up	1.58	RP1-21O18.1	kazrin
212943_at	0.0370	down	-1.66	KIAA0528	KIAA0528
231887_s_at	0.0281	up	1.53	KIAA1274	KIAA1274
208933_s_at	0.0498	down	-1.57	LGALS8	lectin, galactoside-binding, soluble, 8
218577_at	0.0181	down	-1.80	LRRC40	leucine rich repeat containing 40
228583_at	0.0386	down	-1.58	LIN52	lin-52 homolog (C. elegans)
1554455_at	0.0410	down	-1.62	LINS1	lines homolog 1 (Drosophila)
225060_at	0.0409	down	-1.50	LRP11	low density lipoprotein receptor-related protein 11
201721_s_at	0.0174	up	2.18	LAPTM5	lysosomal multispanning membrane protein 5
235374_at	0.0092	down	-1.79	MDH1	Malate dehydrogenase 1, NAD (soluble)
220945_x_at	0.0190	down	-1.56	MANSC1	MANSC domain containing 1
223494_at	0.0461	down	-1.63	MGEA5	meningioma expressed antigen 5 (hyaluronidase)
223578_x_at	0.0200	down	-1.54	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
219220_x_at	0.0334	down	-1.51	MRPS22	mitochondrial ribosomal protein S22
224873_s_at	0.0358	down	-1.54	MRPS25	mitochondrial ribosomal protein S25
225673_at	0.0443	down	-1.63	MYADM	myeloid-associated differentiation marker

227168_at	0.0100	down	-1.81	MIAT	myocardial infarction associated transcript (non-protein coding)
228658_at	0.0455	down	-1.60	MIAT	myocardial infarction associated transcript (non-protein coding)
237322_at	0.0072	down	-1.91	MIAT	myocardial infarction associated transcript (non-protein coding)
229793_at	0.0068	down	-1.62	ASAH2B	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B
221214_s_at	0.0259	up	1.84	NELF	nasal embryonic LHRH factor
208285_at	0.0272	up	1.57	OR7A5	olfactory receptor, family 7, subfamily A, member 5
226574_at	0.0180	down	-1.73	PSPC1	paraspeckle component 1
201397_at	0.0182	up	2.00	PHGDH	phosphoglycerate dehydrogenase
209581_at	0.0487	up	1.74	PLA2G16	phospholipase A2, group XVI
213142_x_at	0.0433	down	-1.65	PION	pigeon homolog (Drosophila)
222150_s_at	0.0238	down	-1.61	PION	pigeon homolog (Drosophila)
214086_s_at	0.0416	down	-1.86	PARP2	poly (ADP-ribose) polymerase 2
208051_s_at	0.0404	down	-1.61	PAIP1	poly(A) binding protein interacting protein 1
224110_at	0.0424	down	-1.51	LOC100133319	PRO1804

202185_at	0.0398	up	1.53	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
219236_at	0.0265	up	2.28	PAQR6	progestin and adipoQ receptor family member VI
222394_at	0.0348	down	-1.60	PDCD6IP	programmed cell death 6 interacting protein
236456_at	0.0463	down	-1.92	PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)
217762_s_at	0.0380	up	1.68	RAB31	RAB31, member RAS oncogene family
224366_s_at	0.0422	down	-1.71	REPS1	RALBP1 associated Eps domain containing 1
214103_s_at	0.0148	up	1.71	RAP2A	RAP2A, member of RAS oncogene family
219303_at	0.0174	down	-1.66	RNF219	ring finger protein 219
229273_at	0.0433	up	1.61	SALL1	sal-like 1 (Drosophila)
215009_s_at	0.0409	down	-1.52	SEC31A	SEC31 homolog A (S. cerevisiae)
1558795_at	0.0249	down	-2.26	LOC728052	similar to hCG2031213
1558796_a_at	0.0093	down	-2.14	LOC728052	similar to hCG2031213
219583_s_at	0.0354	down	-1.90	SPATA7	spermatogenesis associated 7
234929_s_at	0.0410	down	-1.60	SPATA7	spermatogenesis associated 7
1555883_s_at	0.0143	down	-1.50	SPIN3	spindlin family, member 3
221768_at	0.0085	down	-1.94	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract

					binding protein associated)
214954_at	0.0167	down	-2.10	SUSD5	sushi domain containing 5
202813_at	0.0048	down	-1.97	TARBP1	TAR (HIV-1) RNA binding protein 1
1554701_a_at	0.0334	up	1.53	TBC1D16	TBC1 domain family, member 16
213913_s_at	0.0311	down	-1.58	TBC1D30	TBC1 domain family, member 30
238480_at	0.0288	down	-1.53	TTC39C	tetratricopeptide repeat domain 39C
226120_at	0.0286	down	-1.52	TTC8	tetratricopeptide repeat domain 8
200916_at	0.0221	up	1.71	TAGLN2	transgelin 2
225462_at	0.0254	down	-1.56	TMEM128	transmembrane protein 128
236824_at	0.0348	down	-1.54	TMEM132B	transmembrane protein 132B
228054_at	0.0036	down	-1.53	TMEM44	transmembrane protein 44
217766_s_at	0.0479	down	-1.51	TMEM50A	transmembrane protein 50A
221229_s_at	0.0438	down	-1.57	TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)
1560647_at	0.0065	down	-1.58	TSPYL1	TSPY-like 1
1560648_s_at	0.0243	down	-2.26	TSPYL1	TSPY-like 1
224836_at	0.0306	up	2.10	TP53INP2	tumor protein p53 inducible nuclear protein 2

211943_x_at	0.0262	up	1.69	TPT1	tumor protein, translationally-controlled 1
212284_x_at	0.0043	up	1.67	TPT1	tumor protein, translationally-controlled 1
212869_x_at	0.0293	up	1.71	TPT1	tumor protein, translationally-controlled 1
214327_x_at	0.0054	up	1.59	TPT1	tumor protein, translationally-controlled 1
212061_at	0.0283	down	-1.54	SR140	U2-associated SR140 protein
212074_at	0.0203	down	-1.69	UNC84A	unc-84 homolog A (C. elegans)
208626_s_at	0.0083	up	1.87	VAT1	vesicle amine transport protein 1 homolog (T. californica)
201783_s_at	0.0113	up	1.59	RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
230117_at	0.0353	down	-2.00	VSTM2A	V-set and transmembrane domain containing 2A
236308_at	0.0495	down	-1.90	VSTM2A	V-set and transmembrane domain containing 2A
213155_at	0.0066	up	1.69	WSCD1	WSC domain containing 1
1568680_s_at	0.0500	down	-1.50	YTHDC2	YTH domain containing 2
222606_at	0.0323	down	-1.55	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)

1557438_at	0.0232	up	1.73		
1562016_at	0.0194	up	1.51		
1566716_at	0.0197	up	1.66		
1569305_a_at	0.0372	up	1.73		
208276_at	0.0281	up	1.77		
226497_s_at	0.0302	up	1.87		
226579_at	0.0257	up	1.51		
226865_at	0.0258	up	1.62		
227082_at	0.0433	up	1.60		
227565_at	0.0223	up	1.55		
228349_at	0.0145	up	1.52		
228655_at	0.0125	up	1.51		
228807_at	0.0259	up	1.56		
229048_at	0.0285	up	2.22		
229541_at	0.0367	up	1.69		
233479_at	0.0178	up	1.59		
234438_at	0.0168	up	1.62		
235133_at	0.0347	up	1.54		
235617_x_at	0.0445	up	2.29		
235808_at	0.0326	up	1.75		
236576_at	0.0405	up	1.79		
236704_at	0.0129	up	2.16		
237372_at	0.0290	up	1.57		
238298_at	0.0137	up	1.91		
238477_at	0.0075	up	1.51		
241160_at	0.0330	up	1.59		
243272_at	0.0490	up	1.70		

243839_s_at	0.0088	up	1.55		
AFFX-M27830_M_at	0.0417	up	1.95		
1557326_at	0.0199	down	-1.82		
1557475_at	0.0253	down	-2.24		
1557746_at	0.0365	down	-1.53		
1558170_at	0.0412	down	-1.72		
1558672_at	0.0358	down	-1.65		
1563187_at	0.0296	down	-1.58		
1563941_at	0.0029	down	-1.56		
1564358_at	0.0291	down	-1.80		
215423_at	0.0433	down	-1.92		
225197_at	0.0046	down	-1.63		
226341_at	0.0375	down	-1.56		
226343_at	0.0474	down	-1.75		
227126_at	0.0438	down	-1.61		
228013_at	0.0467	down	-1.63		
228792_at	0.0079	down	-1.81		
229193_at	0.0072	down	-1.56		
229384_at	0.0303	down	-1.54		
231329_at	0.0170	down	-1.77		
233185_at	0.0446	down	-1.66		
235561_at	0.0475	down	-1.55		
235613_at	0.0493	down	-1.68		
236089_at	0.0275	down	-1.61		
236143_at	0.0459	down	-1.52		
236261_at	0.0370	down	-1.61		

236468_at	0.0132	down	-1.66		
237015_at	0.0194	down	-1.63		
237400_at	0.0484	down	-1.59		
238191_at	0.0456	down	-1.59		
239278_at	0.0083	down	-1.63		
240503_at	0.0117	down	-1.68		
241807_x_at	0.0342	down	-1.56		
242024_at	0.0284	down	-1.62		
242153_at	0.0266	down	-1.51		
242494_at	0.0350	down	-1.71		
242652_at	0.0425	down	-1.65		
243189_at	0.0208	down	-1.53		